SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: HUMAN MPL LIGAND

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 04-Apr-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 3-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Winter, Daryl B.
(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: P0871P3

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415/225-1249
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
-21 -20                 -15                 -10

Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
     -5                   1                   5

Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
 10                  15                  20

Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
 25                  30                  35

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
 40                  45                  50

Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
 55                  60                  65

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
 70                  75                  80

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
 85                  90                  95

Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
100                 105                 110

Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
115                 120                 125

Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
130                 135                 140

Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
145                 150                 155

Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
160                 165                 170

Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
175                 180                 185
```

C1 cont.

Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
190 195 200

Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
205 210 215

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
220 225 230

Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
235 240 245

Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
250 255 260

Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
265 270 275

Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
280 285 290

Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
295 300 305

Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
310 315 320

C1 cont.

Ser Gln Asn Leu Ser Gln Glu Gly
325 330 332

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1795 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50

CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100

CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150

CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200

GACACCCCGG CCAGA ATG GAG CTG ACT GAA TTG CTC CTC 239
Met Glu Leu Thr Glu Leu Leu Leu
-21 -20 -15

```
GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 278
Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser
            -10                 -5

AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 317
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
  1             5                  10

AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 356
Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
     15                  20                  25

AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 395
Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
            30                  35

CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 434
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys
 40                  45                  50

ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 473
Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly
          55                  60                  65

GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG 512
Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
                70                  75

GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG 551
Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
     80                  85                  90

CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG 590
Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
            95                  100

CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 629
Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg
105                 110                 115

ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC 668
Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser
          120                 125                 130

TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG 707
Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
                135                 140

CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC CCA 746
Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro
    145                 150                 155
```

C' cont

```
CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC 785
Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu
            160                 165

ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG 824
Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu
170                 175                 180

GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT 863
Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
        185                 190                 195

GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT 902
Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile
                200                 205

CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA 941
Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln
    210                 215                 220

ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT 980
Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
            225                 230

GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC 1019
Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr
235                 240                 245

CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA 1058
Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr
        250                 255                 260

GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT 1097
Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro
                265                 270

TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT ACG CTC TTC 1136
Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe
    275                 280                 285

CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC 1175
Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu
            290                 295

CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC 1214
His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr
300                 305                 310

CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1253
Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser
        315                 320                 325
```

C' cont.

CAG AAT CTG TCT CAG GAA GGG T AAGGT TCTCAGACAC 1290
Gln Asn Leu Ser Gln Glu Gly
330 332

TGCCGACATC AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC 1340

CCTGGGAGAC AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC 1390

CCTGGTAAAA GGGATACACA GGACTGAAAA GGGAATCATT TTTCACTGTA 1440

CATTATAAAC CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC 1490

AGAGCAGCTA GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG 1540

ATTCTCTACA TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG 1590

CCTGGCAGTT GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA 1640

AAGGGTAATT TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC 1690

CCTTTACTAT CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC 1740

TTTACTCTTG AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA 1790

AAAAA 1795

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
-16 -15 -10 -5

Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1 5 10

Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25 26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50

CACCTCTCCT CATCTAAGAA   TTG CTC CTC GTG GTC ATG CTT 91
                        Leu Leu Leu Val Val Met Leu
                        -16 -15                 -10

CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130
Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro
                  -5                    1

CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169
Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg
  5                  10                  15

GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210
Asp Ser His Val Leu His Ser Arg Leu
         20                  25  26

CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260

GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310

TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360

ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
TCTAGACGAG AGCTTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50

TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100

GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150

TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200

GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250

CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300
```

AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350

ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
35 40 45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
50 55 60

Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
65 70 75

C' cont.

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
80 85 90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
95 100 105

Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
110 115 120

His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu
125 130 135

Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu
140 145 150

Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr
155 160 165

Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly
170 175 180

Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
185 190 195

Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly
200 205 210

Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr
215 220 225

Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe
230 235 240

Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser
245 250 255

Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly
260 265 270

Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu
275 280 285

Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His
290 295 300

Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser
305 310 315

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln
320 325 330

Glu Gly
332

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
1 5 10 15

Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
20 25 30

Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
35 40 45

Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
50 55 60

Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
65 70 75

Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
80 85 90

Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
95 100 105

Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
110 115 120

Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
125 130 135

Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
140 145 150

Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
155 160 165

Arg
166

(2) INFORMATION FOR SEQ ID NO:8:

C' cont.

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1443 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50

AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100

ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGA ATG GAG 143
Met Glu
-21 -20

CTG ACT GAT TTG CTC CTG GCG GCC ATG CTT CTT GCA GTG 182
Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
-15 -10

GCA AGA CTA ACT CTG TCC AGC CCC GTA GCT CCT GCC TGT 221
Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys
-5 1 5

```
GAC CCC AGA CTC CTA AAT AAA CTG CTG CGT GAC TCC CAC 260
Asp Pro Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His
          10                  15                  20

CTC CTT CAC AGC CGA CTG AGT CAG TGT CCC GAC GTC GAC 299
Leu Leu His Ser Arg Leu Ser Gln Cys Pro Asp Val Asp
                  25                  30

CCT TTG TCT ATC CCT GTT CTG CTG CCT GCT GTG GAC TTT 338
Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp Phe
      35                  40                  45

AGC CTG GGA GAA TGG AAA ACC CAG ACG GAA CAG AGC AAG 377
Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys
              50                  55

GCA CAG GAC ATT CTA GGG GCA GTG TCC CTT CTA CTG GAG 416
Ala Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu
 60                  65                  70

GGA GTG ATG GCA GCA CGA GGA CAG TTG GAA CCC TCC TGC 455
Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys
          75                  80                  85

CTC TCA TCC CTC CTG GGA CAG CTT TCT GGG CAG GTT CGC 494
Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg
                  90                  95

CTC CTC TTG GGG GCC CTG CAG GGC CTC CTA GGA ACC CAG 533
Leu Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln
      100                 105                 110

GGC AGG ACC ACA GCT CAC AAG GAC CCC AAT GCC CTC TTC 572
Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe
              115                 120

TTG AGC TTG CAA CAA CTG CTT CGG GGA AAG GTG CGC TTC 611
Leu Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe
125                 130                 135

CTG CTT CTG GTA GAA GGT CCC ACC CTC TGT GTC AGA CGG 650
Leu Leu Leu Val Glu Gly Pro Thr Leu Cys Val Arg Arg
          140                 145                 150

ACC CTG CCA ACC ACA GCT GTC CCA AGC AGT ACT TCT CAA 689
Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr Ser Gln
                  155                 160

CTC CTC ACA CTA AAC AAG TTC CCA AAC AGG ACT TCT GGA 728
Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly
      165                 170                 175
```

C' cont.

```
TTG TTG GAG ACG AAC TTC AGT GTC ACA GCC AGA ACT GCT 767
Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala
            180                 185

GGC CCT GGA CTT CTG AGC AGG CTT CAG GGA TTC AGA GTC 806
Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val
190                 195                 200

AAG ATT ACT CCT GGT CAG CTA AAT CAA ACC TCC AGG TCC 845
Lys Ile Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser
        205                 210                 215

CCA GTC CAA ATC TCT GGA TAC CTG AAC AGG ACA CAC GGA 884
Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly
                220                 225

CCT GTG AAT GGA ACT CAT GGG CTC TTT GCT GGA ACC TCA 923
Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser
    230                 235                 240

CTT CAG ACC CTG GAA GCC TCA GAC ATC TCG CCC GGA GCT 962
Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala
            245                 250

TTC AAC AAA GGC TCC CTG GCA TTC AAC CTC CAG GGT GGA 1001
Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly Gly
255                 260                 265

CTT CCT CCT TCT CCA AGC CTT GCT CCT GAT GGA CAC ACA 1040
Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His Thr
        270                 275                 280

CCC TTC CCT CCT TCA CCT GCC TTG CCC ACC ACC CAT GGA 1079
Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly
                285                 290

TCT CCA CCC CAG CTC CAC CCC CTG TTT CCT GAC CCT TCC 1118
Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser
    295                 300                 305

ACC ACC ATG CCT AAC TCT ACC GCC CCT CAT CCA GTC ACA 1157
Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr
            310                 315

ATG TAC CCT CAT CCC AGG AAT TTG TCT CAG GAA ACA TAGCGC 1199
Met Tyr Pro His Pro Arg Asn Leu Ser Gln Glu Thr
320                 325                 330 331

G GGCACTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC 1240

AAGCTTCCCC AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT 1290
```

C1 cont

GCTTTCACCT AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT 1340

AAAATTTTAG GAGCTATTTT TTTTTAACCT ATCAGCAATA TTCATCAGAG 1390

CAGCTAGCGA TCTTTGGTCT ATTTTCGGTA TAAATTTGAA AATCACTAAT 1440

TCT 1443

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
-21 -20 -15 -10

Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
-5 1 5

Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
10 15 20

C' cont. Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
25 30 35

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50

Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
55 60 65

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
70 75 80

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85 90 95

Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Gly Arg Thr
100 105 110

Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln
115 120 125

Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro
130 135 140

Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser
145 150 155

Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr
160 165 170

Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala
175 180 185

Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile
190 195 200

Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile
205 210 215

Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His
220 225 230

Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp
235 240 245

Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu
250 255 260

Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His
265 270 275

Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser
280 285 290

c' cont.

Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met
295 300 305

Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro
310 315 320

Arg Asn Leu Ser Gln Glu Thr
325 330 331

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp
35 40 45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala
50 55 60

Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu Gly Val Met
65 70 75

Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu
80 85 90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
95 100 105

Gly Leu Leu Gly Thr Gln Gly Arg Thr Thr Ala His Lys Asp Pro
110 115 120

Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu Arg Gly Lys Val
125 130 135

Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu Cys Val Arg Arg
140 145 150

Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr Ser Gln Leu Leu
155 160 165

C' cont.

Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr
170 175 180

Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser
185 190 195

Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly Gln Leu Asn
200 205 210

Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg
215 220 225

Thr His Gly Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr
230 235 240

Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe
245 250 255

Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro
260 265 270

Ser Pro Ser Leu Ala Pro Asp Gly His Thr Pro Phe Pro Pro Ser
275 280 285

Pro Ala Leu Pro Thr Thr His Gly Ser Pro Pro Gln Leu His Pro
290 295 300

Leu Phe Pro Asp Pro Ser Thr Thr Met Pro Asn Ser Thr Ala Pro
305 310 315

His Pro Val Thr Met Tyr Pro His Pro Arg Asn Leu Ser Gln Glu
320 325 330

Thr
331

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp Xaa Val Leu His Gly Arg Leu
20 25 26

C1 cont.

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Arg Leu Leu Asn Lys Leu Leu Arg
1 5 9

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

C1 cont.

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCNGCNCCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

NCCRTGNARN ACRTGRTCRT C 21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

TGACCACGTT CAGCACGGC 69

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

C' cont.

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGACCACGTC CATCACGGC 69

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAGTCTGCCG TGAAGGACAT GG 22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

C' cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu His
20 23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro
1 5 10 15

Val Leu Leu Pro Ala Val Asp Phe
20 23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
1 5 10 15

Asp Ile Leu Gly Ala Val Thr Leu
20 23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
1 5 10 15

Cys Leu Ser Ser Leu
20

Cont.

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
1 5 10 15

Gln Ser Leu
18

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys
1 5 10 15

Asp Pro Asn Ala Ile Phe
20 21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
1 5 10 15

Leu Val Gly Gly Ser Thr Leu Cys Val Arg
20 25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

C' cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp His Val Leu His Gly Arg
20 25